



REPLACEMENT SHEET

Applicant(s): Roy A. Gravel et al.

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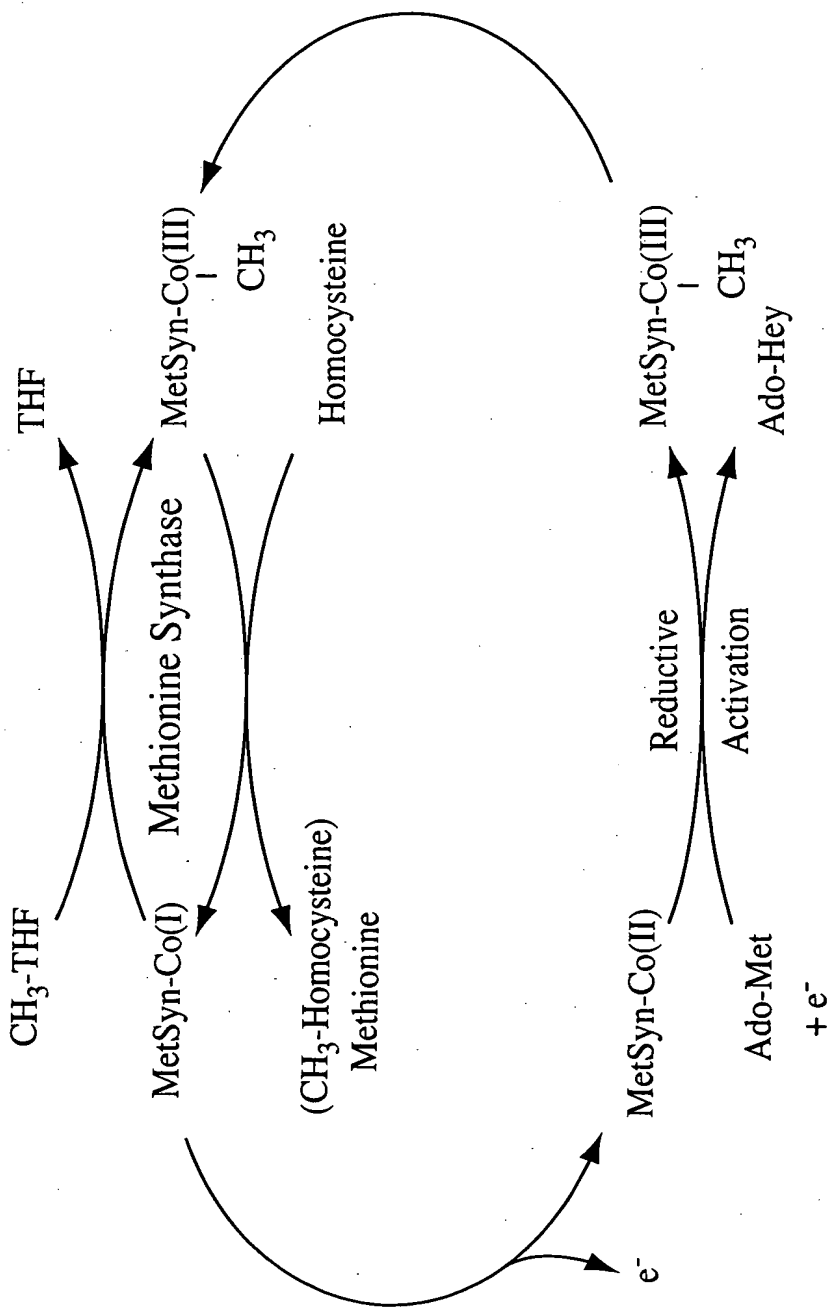


Fig. 1

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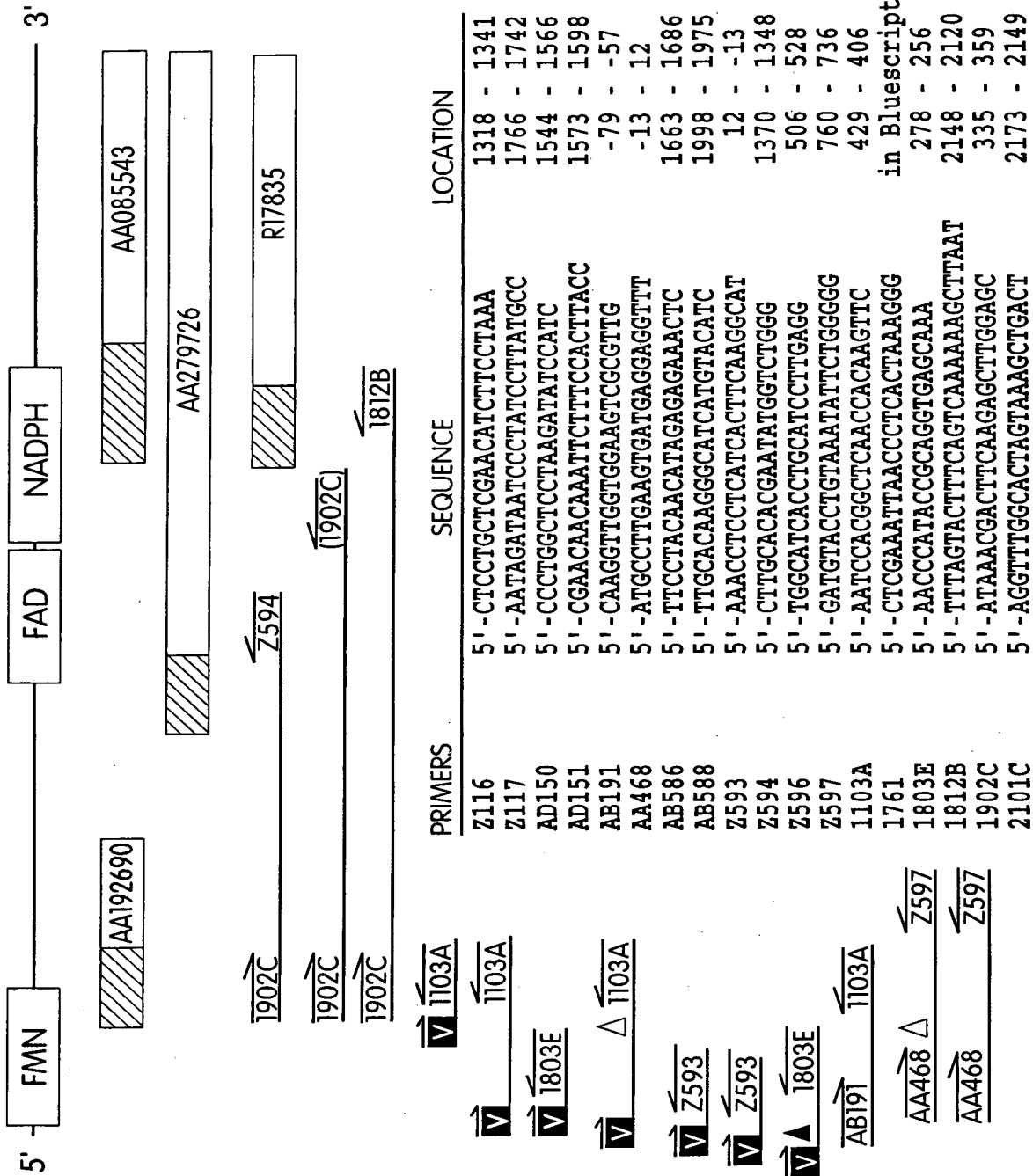


Fig. 2

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CAAGTTGGTGAAGTCGGCTTGTGCAGGTTCTGTCGCCGCTGGCGGGGCTGTTTCACTGTTACATGCTTGAAGTG

1 ATGAGGAGGTTTCTGTTACTATATGCTACAGCAGGACAGGCAAGGCCATCGCAGAGAAATCTGTGAGCAAGCTGTGGTACATGATTTCTGCAGATCTTCACTGTAATTAGTGAA
M R R F L L L Y A T Q Q Q G Q A K A I A E E M C E Q A V V H G F S A D L H C I S E 40

121 TCCGATAGATGACTAAACCGAAACAGCTCCCTTGTGTTTCTACACGGGACCGGAGACCCACCCGACACAGCCCGCAAGTTTGTTAAGGAATAACAGAACCAACA
S D K Y D L K T E T A P L V V V S T T G T G D P D T A R K F V K E I Q N Q T 80

241 CTCGCCGTTGATTTCTTTGCTCACCTCGGATGGGTTACTGGGTCGTGGTATTCAGAAATACACCTACTTTTGCATTTGGGGGGAAGATAATTGATAAACGACTTCAAGAGCTTGGAGCC
L P V D F F A H L R Y G L L G L G D S E Y T Y F C N G G K I I D K R L Q E L G A 120

361 CGGCATTTCTATGACACTGGACATGCAGATGACTGTGTAGGTTAGAACTTGTGGCTGTGGATCTGGCCAGGCTCTCAGAAAGCATTTTAGGTCAAGCAGCAGGACAA
R H F Y D T G H A D D C V G L E L V V E P W I A G L W P A L R K H F R S S R G Q 160

481 GAGGAGATAAGTGGGCACTCCCGTGGCACTCCCTGGAATCACTTCTGAGGACAGACCTTGTGAAGTCAGAGTGCTACACATTTCAAGTCGAGCTTCTGAGATTCGATTCAGGA
E E I S G A L P V A S P A S L R T D L V K S E L L H I E S Q V E L L R F D D S G 200

601 AGAAAGATTCGAGGTTTGAAGCAAAATGCAGTGAACAGCAACCAATCCAATGTTGTAATTGAAGACHTTGTGTCCTCACTTACCCGTTGGTACCCCACTCTCACAGGCTCTCTG
R K D S E V L K Q N A V N S N Q S N V V I E D F E S S L T R S V P L S Q A S L 240

721 AATATTCTGTTTACCCCAAGAAATTTACAGGTACATCTGCAGGAGTCTCTGGCCAGGAGGAAAGCCAAAGTATCTGTGACTTCAGCAGATCCAGTTTTTCAAGTGCCTTCAAG
N I P G L P P E Y L Q V H L Q E S L G Q E E S Q V S V T S A D P V F Q V P I S K 280

841 GCAGTTCAACTTACTAGGAATGATGCCATAAAACCACTCTGCTGGTAGAATTGGACATTTCAAATACAGACTTTTCTATCAGCCTGGAGATGCCCTTCAGCGTGATCTGCCCTAACAGT
A V Q L T T N D A I K T T L L V E L D I S N T D F S Y Q P G D A F S V I C P N S 320

961 GATTTGAGGTACAAAGCTTACTCCAAAGACTGCAGCTTGAAGATAAAGAGAGCACTGGCTCCCTTTTGAATAATAAGGACAGACACAAAGAAAGAGGAGTACCTTACCCCAAGCATATA
D S E V Q S L L Q R L Q L E D K R E H C V L L K I K A D T K K G A T L P Q H I 360

1081 CCTGGGGATGTTCTCTCCAGTTCAATTTTACCTGTGTCTGTGAATCCGAGCAATTTCTTAAAGCAATTTTGGAGCCCTTGTGGACTATACCAGTGACAGTGCTGAAAGCGCAGG
P A G C S L Q F I F T W C L E I R A I P K K A F L R A L V D Y T S D S A E K R R 400

1201 CTCAGAGCTGTGAGTAACAAGGGGACCGGATTATAGCCGTTTGTACGAGATGCCGTGTGCTGCTTGTGGATCTCTCTCGCTTCCCTTCTTGGCAGCCACCACTCAGTCTC
L Q E L C S K Q G A A D Y S R F V R D A C A C L L D L L L A F P S C Q P P L S L 440

Fig. 3-1

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1321 CTGCTCGAACATCTTCCATAAATTCAACCCAGACCATATTGCTGTGCAAGCTCAAGTTTATTACCCAGGAAGCTCCATTGTCTTCAACATTGTGGAATTTCTGTCTACTGCCACA
L L E H L P K L Q P R P Y S C A S S L F H P G K L H F V F N I V E F L S T A T 480
1441 ACAGAGGTTCTGGGAAGGAGTATGTACAGGCTGGCTGGCTTGTGTGCTTCAAGTTCAGCAACATACATGCAATCCCATGAAGACACGGGAAAGCCCTGGCTCCTTAAGATA
T E V L R K G V C T G W L A L L V A S V L Q P N I H A S H E D S G K A L A P K I 520
1561 TCCATCTCTCTGCAACACAAATTTCTTCCACTTACAGATGACCCCTCAATCCCATCATATAATGGTGGTCCAGGAACCGGCATAGCCCGTTATTGGGTTCTCTACAACATAGAGAG
S I S P R T T N S F H L P D D P S I P I M V G P G T G I A P F I G F L Q H R E 560
1681 AAATCCAGAACACACCCAGATGGAAATTTTGGAGCAATGTGGTGTGCTGAGGCAATAGGATAGGATTATCTATTCAAAAAGAGCTCAGACATTTCTTAAAGCATGGG
K L Q E Q H P D G N F G A M W L F F G C R H K D R D Y L F R K E L R H F L K H G 600
1801 ATCTTAATCACTAAAGTTTCTTCAAGAGATGCTCCTGTGGGAGGAGGAAGCCCGAGCAAGTATGTACAGACACATCCAGCTTCATGGCCAGCAGGTGGCGGAGAAATCCTC
I L T H L K V S F S R D A P V G E E A P A K Y V Q D N I Q L H G Q Q V A R I L 640
1921 CTCCAGGAGAACGGCCATATTTATGTGTGGAGATGCAAGAATATGGCCAGCATGTACATGATGCCCTGTGCAATAATAAGCAAGAGTTGGAGTTGAAAACTAGAAAGCAATG
L Q E N G H I Y V C G D A K N M A K D V H D A L V Q I I S K E V G V E K L E A M 680
2041 AAAACCTGGCCACTTTAAAGAGAAACGCTACCTTCAGGATATTTGGTCAATAAACAGAAATTAAGAAAGAGGATTAAAGCTTTTGTGACTGAAAGTACTAAAGTCAGCTTTAC
K T L A T L K E E K R Y L Q D I W S ***
2161 TAGTGCCAAACCTTTAAATTTCAAAGAAATTTCTTTCAACATTTCTTGAAGGACATGGAGATTGGATCATTTAAACAATAAACAACCTTCTCTGATTTGATTTACGTATC
2281 TTCTATCTAGCGCCTTCTGTGCTGTGACTCTCCCAATTTGCCCTGTGCTTCTGAGCTTAAAGGAGCCTTCTGAGTCCCTATCAGCGCCTCTTACTTCCAGAGAACT
2401 TCACAGAGACTCTGTCTTCCATGCAAGGCTTCTGAAATAGGGAGACTGACTGAGTACTCATCTTGTGACCTTACAGTCCCAACATTTAAAAAGATGAAATGATTTATTTTA
2521 TATGATGTATACCCATAAAGATGCTCATATTAATGTACTTAATTAACATGTAGAGCATATCTGTTATGTATGTTAATCAATGGTTATTTGTACTAAAGCTATATTTCTG
2641 ATAAAAATATTTAGGATAATTTGCCATACAGAGGATTTATTTTATGATGCTGGGAAATATGAATGTATTTTAAATTTCACTCTGGGCATATGGATTTTATCTATCACCATTACTTTT
2761 TTTTAAAGTCACAATTTTGGACATTTTGGACATTTGCAATTTACAGTACCAGTACGTACATATTTTAAAGAAAGATACAACCTTTTATTTTCACTCCTTTTATTTCTGTGCTT
2881 GGCACATTTTGGATTTTCCACATTTATTTGCTCCATGATACCACTCAAGCAGTGTGCTGGACCTAAATACTGACTTAGTATCCTTGGATTTTAGATTTCCCCAGTGTCTAAT
3001 TCCCTGTTATTAATTTGCACAAACAAATGTTATGATATCTTTCTCCACTGTTCTTAATATATATTTTATTTTATTTGATAGCTTGGGATTTAAACATCTCTCTGTGAGGCTTT
3121 TGATCCTTTTGAGAAATAAAGATCTGAAAGAAATGGCATATCTTAAAAAAAATAAAAAA

Fig. 3-2

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Fig. 3-3

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1321 CTGTCGAACATCTTCCCTAACTTCAACCCAGACCATATTCCTGTGCAAGCTCAAGTTTATTTCCACCCAGGAAGCTCCATTTTGTCTTCAACATTTGTGGAATTTCTGTCTACTGCCACA
L L E H L P K L Q P R P Y S C A S S L F H P G K L H F V F N I V E F L S T A T 480

1441 ACAGAGTTCTGCGAAGGAGTATGTACAGGCTGGCTGGCTTGTGGTCTTCAAGTTCTTCAAGCAACATACATGATCCCATGAACACAGCGGGAAGCCCTGGCTCCTAAGATA
T E V L R K G V C T G W L A L L V A S V L Q P N I H A S H E D S G K A L A P K I 520

1561 TCCATCTCTCTCGAACACAAATTTTCCACTTACCAGATGACCCCTCAATCCCATCAATATGGTGGTCAGGAACCGGCATAGCCCGTTTATTTGGTTCTTACAAACATAGAGAG
S I S P R T T N S F H L P D D P S I P I I M V G P G T G I A P F I G F L Q H R E 560

1681 AAATCCAAAGAACACACCAGATGGAATTTTGGACAAATGTGGTGTGGTGGTCCAGGCATAGGATAGGATTTCTATTCAGAAAAGAGGTCAGACATTTCTTAAAGCATGGG
K L Q E Q H P D G N F G A M W L F F G C R H K D R D Y L F R K E L R H F L K H G 600

1801 ATCTTAATCTCTAAAGTTTCTTCTCAAGAGATGCTCTCTGTTGGGAGGAGGAGAGCCCGAGCAAGTATGACAGCAACATCCAGTTTCATGCCCAGAGGTGGCGAGAAATCCTC
I L T H L K V S F S R D A P V G E E A P A K Y V Q D N I Q L H G Q Q V A R I L 640

1921 CTCAGGAGAACGGCCATATTTATGTGTGGAGATGCAAGAATATGGCAAGATGTACATGATGCCCTTGTGCAATTAATAAGCAAGAGTTTGAGTTGAAAACTAGAACGAATG
L Q E N G H I Y V C G D A K N M A K D V H D A L V Q I I S K E V G V E K L E A M 680

2041 AAAACCCCTGGCCACTTTAAAGAGAAAGAAACGCTACCTTCAGGATATTTGGTCATATAAACAGAAATTAAGAAAGAGGATTAAGCTTTTTTGTGACTGAAAGTAAAGTCAGCTTTAC
K T L A T L K E E K R Y L Q D I W S ***

2161 TAGTGCCAAACCTTTAAATTTCAAAGAAATTTCTTCAACATTTCTTGAAGACATGGAGTGGAGATTTGATCATTTAAACAATAAACAACCTTCTGATTTGATTTTACGTATC
2281 TTCTATCTACGCCCTTCTGTGCTGTGACTCTCCCAATTTGCCCTGTTCGCTTGTGAGCTCTTCTGAGCTAAAGCAGCCTTCAGTCCCTATCAGCGCTCTCTTACTTCCAGAGAACT
2401 TCACAGAGACTCTGTCTCCATGCAAGGCTTCCATGAAATAGGGAGACTGACTGAGTAGCTTCTGTGACTTACAGTGCCAAACATTTAAAGATATGAAATGATTTATTTTAA
2521 TATGATGTATACCCATAAGAAATGCTCATATTAATGCTACTTAAATPACACATGTACAGCATATCTGTTATATGTTTATGTAACATCAAAATGGTTATTTGTTACTAAAGTATATTTCTG
2641 ATAAAAATATTTTAGGATAATTCCTACAGAGGATTTATTTTATGATGCTGGAAATATGAATGATTTTAAATTTCACTCTGGGATATGGATTTATCTATCACCATTACTTTT
2761 TTTTAACTCACAATTTTGGACATTTTGGACATTTTCAATTTTACAGTACCAGTACATATTTTAAAGAAATACAACTTTTATTTTCACTCTCTTTTATTTCTGCTGCTT
2881 GGACATTTTGTAGTTTCCCAATTTTGTCTCCATGATACCACTCAAGAGTGTGCACTAAATACTGACTTTAGTAGTATCTTGGATTTTGTAGTTTCCAGAGTGTCTTAAT
3001 TCCTGTATATTTGGACAAACAAATGTTATGATTAATTTTCTCCACTGTCTTAATATATTTTATTTGATGCTTGGGATTTTAAACATCTCTGTGTGAAGGCTTT
3121 TGATCCTTTTGAAATTAAGATCTGAAGAAATGGCATATCTTAAAAAATAAAAAA

Fig. 3-4

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HsMTRR	-----	
CeMTRR	-----	
HsCPR	MGDSHVDTSSSTVSEAVAEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEE	50
	FMN	
HsMTRR	-----MRRFLLLYATQQGQAKAIAEEMCE	24
CeMTRR	-----MTDFLIAFGSQTGQAETIAKSLKE	24
HsCPR	VPEFTKIQTLTSSVRESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSK	100
 * * * * .	
	FMN	
HsMTRR	QAVVHGFSADLHCISESDK-YDLKT-----ETAPLVVVVSTTGTGDPP	66
CeMTRR	KAELIGLTPRLHALDENEEKFNLE-----EKLC-AIVVSSTGDGDAP	66
HsCPR	DAHRYG---MRGMSADPEEYDLADLSSLPIDNALVVFCMATYGEDPT	146
	* * * * * *	
	FMN	
HsMTRR	DTARKFVKEIQNTLPVDFFAHLRYGLLGLGDSEYTYFCNGGKIIDKRLQ	116
CeMTRR	DNCARFVRRINRNSLENEYLNLDYVLLGLGDSNYSSYQTI PRKIDKQLT	116
HsCPR	DNAQDFYDWLQETDVD---LSGVKFAVFGLGNKTYEHFNAMGKYVDKRLE	193
	* * * * * * .	
HsMTRR	ELGARHFYDTGHADDCVGLLELVVEPWIALGLWPALRKHFRRSSRGQEEISGA	166
CeMTRR	ALGANRLFDRAEADDQVGLLEVEPWIEKFFATLASRFDISADKMN----	162
HsCPR	QLGAQRIFELGLGDDDGNDLEEDFITWREQFWPAVCEHF-----GV	233
	*** ** * * . . *	
HsMTRR	LPVASPASLRTDLVKSELLHIESQVELL--RFDDSGRKDSEVLKQNAVNS	214
CeMTRR	-AITESSNLKLNQVKTE----EEKKALLQKRIEEDSDEGRGRVIGID-	206
HsCPR	EATGEESSIRQYEL-----VVHTDIDAQVYMGMGRLLKSYEN	271
	
HsMTRR	NQSNVVIEDF---ESSLTRSVPLS-QASLNIPGLPPEYLQVHLQESLGQ	260
CeMTRR	---MLIPEHYDYPEISLLKGSQTLSDENLRVPIAPQPPFIVSSVSNRKLP	253
HsCPR	QKP-----PFD-----AKNPFLAAVTTNRKLN	293
	
HsMTRR	EESQVS-----VTSADPVFQVPISKAVQLTT--NDAIKTTLLVELDIS	301
CeMTRR	EDTKLEWQNLCKMPGVVTKPFEVLVVSAEFVTDPFSSKKIKTKRMITVDFG	303
HsCPR	QGTE-----RHLMHLELD	306
	
HsMTRR	N--TDFSYQPGDAFSVICPNSDSEVQSLLQR-LQLEDKREHCVLLKIKAD	348
CeMTRR	DHAAELQYEPGDALFYFCVNPALVNFILKRCGVLDIADQQCEL-SINPK	352
HsCPR	ISDSKIRYESGDHVAVYPANDSALVNQLGK---ILGADLD--VMSLNNL	351
	. * . ** * * . * . . .	
HsMTRR	TKKKGATLPQHIPAGCSLQFIFTWCLEIRAI PKKAFLRALVDYTSDSA EK	398
CeMTRR	TEKINAQIPGHVHKITTLRHMFTTCLDIRRAPGRPLIRVLAESTSDPNEK	402
HsCPR	DEESNKKHP--FPCPTSRYRTALTYILDITNPPRTNVLYELA QYASEPSEQ	399
	* * * * * .	

Fig. 4-1

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HsMTRR	RRLQEL--CSKQGAADYSRFVRDACACLLDLLLAFPPSCQPPLSLLLEHLP	446
CeMTRR	RRLLEL--CSAQGMKDFDTDFVRTPGLSLADMLFAFPNVKPPVDRLIELLP	450
HsCPR	ELLRKMASSSGEGKELYLSWVVEARRHILAILQDCPSLRPPIDHLCCELLP	449
	* . * . * . . * . . * * * * *	
	FAD FAD FAD	
HsMTRR	KLQPRPYSCASSSLFHPGKLHFVFNIVEFLSTATTEVLRKGVCTGWLALL	496
CeMTRR	RLIPRPYSMSS---YENRKARLIYSEMEFPATDGRRHSRKGLATDWLNSL	497
HsCPR	RLQARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL---	494
	* * * * * . * . * * *	
HsMTRR	VASVLQPNIHASHEDSGKALAPKISISPRTTNSFHLP-----DDPSIP	539
CeMTRR	R-----IGDKVQVLGKEPARFRLPPLGMTKNSAGKLP	529
HsCPR	RAKE-----PVGENGGRALVPMFVRKSQFRLPFK-----ATTP	527
	* *	
	NADPH	
HsMTRR	IIMVGPGTGIAPFIGFLQHREKLQEHPDGNFGAMW-LFFGCRHKDRDYL	588
CeMTRR	LLMVGPGTGVSVFLSFLHFLRKLKQDSPSDFVDVPRVLFPGCRDSSVDAI	579
HsCPR	VIMVGPGTGVAPFIGFIQERAWLRQQGKE---VGETLLYYGCRRSDEDYL	574
	..*****.. * . * . * .. * .. * .	
	NADPH NADPH	
HsMTRR	FRKELRHFLKHGILTHLKVFSFSRDAPVGEEEAPAKYVQDNIQLHGQQVAR	638
CeMTRR	YMSELEMFVSEGILTDLIICESEQ-----KGERVQDGLRKYLDKVLP	621
HsCPR	YREELAQFHRDGALTQLNVAFSRE-----QSHKVYVQHLLKQDREHLWK	618
	. ** * * * * . * * ** . . .	
	NADPH	
HsMTRR	ILLQE-NGHIYVCGDAKNMAKDVHDLVQIISKEVGVEKLEAMKTLATLK	687
CeMTRR	FLTASTESKIFICGDAKGMSKDVWQCFSDIVASDQGIPDLEAKKKLMDLK	671
HsCPR	LI--EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQAVDYIKKLM	666
	. * ..*****. * ..* . * * . *	
	NADPH/FAD	
HsMTRR	EEKRYLQDIWS	698
CeMTRR	KSDQYIEDVWG	682
HsCPR	TKGRYSLDVWS	677
	* * *	

Fig. 4-2

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HsMTRR	-----	
CeMTRR	-----	
HsCPR	MGDSHVDTSSSTVSEAVAEVSLFSMTDMILFSLIVGLLTYWFLFRKKKEE	50
	FMN	
HsMTRR	-----MRRFLLLYATQOQQAIAEEMCE	24
CeMTRR	-----MTDFLIAFGSQTGQAETIAKSLKE	24
HsCPR	VPEFTKIQTLTSSVRESSFVEKMKKTGRNIIVFYGSQTGTAEFANRLSK	100
 * * * * .	
	FMN	
HsMTRR	QAVVHGFSADLHCISESDK-YDLKT-----ETAPLVVVVSTTGTGDPP	66
CeMTRR	KAELIGLTPRLHALDENEKKFNLNE-----EKLC-AIVVSSTGDGDAP	66
HsCPR	DAHRYG----MRGMSADPEEYDLADLSSLPEIDNALVVFCMATYGEDPT	146
	* * * * * *	
	FMN	
HsMTRR	DTARKFVKEIQNTLPVDFFAHLRYGLLGLGDSEYTYFCNGGKIIDKRLQ	116
CeMTRR	DNCARFVRRINRNSLENEYLNLDYVLLGLGDSNYSSYQTIPIRKIDKQLT	116
HsCPR	DNAQDFYDWLQETDVD---LSGVKFAVFGLGNKTYEHFNAMGKYVDKRLE	193
	* * * * * . * . . . * * *	
HsMTRR	ELGARHFYDTGHADDCVGLLELVVEPWIALGLWPALRKHFSSRGQEEISGA	166
CeMTRR	ALGANRLFDRAEADDQVGLELEVEPWIEKFFATLASRFDISADKMN----	162
HsCPR	QLGAQRIFELGLGDDDGNDLEEDFITWREQFWPAVCEHF-----GV	233
	*** * * * * *	
HsMTRR	LPVASPASLRDLDLVKSELLHIESQVELL--RFDDSGRKDSEVLKQNAVNS	214
CeMTRR	-AITESSNLKLNQVKTE----EEKKALLQKRIEDEESDDEGRGRVIGID-	206
HsCPR	EATGEESSIRQYEL-----VVHTDIDAAKVYMGEMGRKLSYEN	271
	
HsMTRR	NQSNVVEDF---ESSLTRSVPLS-QASLNIPGLPPEYLQVHLQESLQ	260
CeMTRR	---MLIPEHYDYPEISLLKGSQTLSDENLRVPIAPQPFIVSSVSNRKLP	253
HsCPR	QKP-----PFD-----AKNPFLAAVTTNRKLN	293
	
HsMTRR	EESQVS-----VTSADPVFQVPISKAVQLTT--NDAIKTTLLVELDIS	301
CeMTRR	EDTKLEWQNLCKMPGVVTKPFEVLVVSFAEFVTDPFSSKIKTKRMITVDFG	303
HsCPR	QGTE-----RHLMHLELD	306
	
HsMTRR	N--TDFSYQPGDAFSVICPNSDSEVQSLLQR-LQLEDKREHCVLLKIKAD	348
CeMTRR	DHAAELQYEPGDAIYFCVPNPALVNFILKRCGVLDIADQOCEL-SINPK	352
HsCPR	ISDSKIRYESGDHVAVYPANDSALVNQLGK--ILGADLD--VVMSSLNNL	351
	. * . * * * * *	
HsMTRR	TKKKGATLPQHIPAGCSLQFIFTWCLEIRAI PKKAFLRALVDYTSDSA EK	398
CeMTRR	TEKINAQIPGHVHKITTLRHMTTCLDIRRAPGRPLIRVLAESTSDPNEK	402
HsCPR	DEESNKKHP--FPCPTSYRTALTYLDITNPRTNVLYELAQYASEPSEQ	399
	* * * * * . * . . . * *	

Fig. 4-3

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HsMTRR	RRLQEL--CSKQGAADYSRFVRDACACLLDLLLAFSPCQPPLSLLLEHLP	446
CeMTRR	RRLLEL--CSAQGMKDFTFVTRTPGLSLADMLFAFPNVKPPVDRLIELLP	450
HsCPR	ELLRKMASSSGEGKELYLSWVVEARRHILAILQDCPSLRPPIDHLCCELLP	449
	* . * . * . * . * * * * *	
	FAD FAD FAD	
HsMTRR	KLQPRPYSCASSSLFHPGKLHVFVNIVEFLSTATTEVLRKGVCTGWLALL	496
CeMTRR	RLIPRPYSMSS---YENRKARLIYSEMEFPATDGRRHRSRKGLATDWLNSL	497
HsCPR	RLQARYYSIASSSKVHPNSVHICAVVVEYETKAGR--INKGVATNWL---	494
	. * * * * . * . * * *	
HsMTRR	VASVLQPNIHASHEDSGKALAPKISISPRTTNSFHLP-----DDPSIP	539
CeMTRR	R-----IGDKVQVLGKEPARFRLPPLGMTKNSAGKLP	529
HsCPR	RAKE-----PVGENGGRALVPMFVRKSQFRLPFK-----ATTP	527
	* *	
	NADPH	
HsMTRR	IIMVGPGTGIAPFIGFLOHREKLQEQHPDGNFGAMW-LFFGCRHKDRDYL	588
CeMTRR	LLMVGPGTGVSVFLSFLHFLRKLKQDSPSDFVDVPRVLFFGCRDSSVDAI	579
HsCPR	VIMVGPGTGVAPFIGFIQERAWLRQQGKE---VGETLLYYGCRRSDEDYL	574
	..*****. * . * . * .. * ..*	
	NADPH NADPH	
HsMTRR	FRKELRHFLKHGILTHLKVFSRDAPVGEEAPAKYVQDNIQLHGQOVAR	638
CeMTRR	YMSELEMFVSEGILTDLIICESEQ-----KGERVQDGLRKYLDKVL	621
HsCPR	YREELAQFHRDGALTQLNVAFSRE-----QSHKVYVQHLLKQDREHLWK	618
	. ** * * * * . * *	
	NADPH	
HsMTRR	ILLQE-NGHIYVCGDAKNMAKDVEDALVQIISKEVGVEKLEAMKTLATLK	687
CeMTRR	FLTASTESKIFICGDAKGMSKDVWQCFSDIVASDQGIPLDLEAKKKLMDLK	671
HsCPR	LI--EGGAHIYVCGDARNMARDVQNTFYDIVAELGAMEHAQAVDYIKKLM	666
	. * ..*****. * ..* . * .. . * . *	
	NADPH/FAD	
HsMTRR	EEKRYLQDIWS	698
CeMTRR	KSDQYIEDVWG	682
HsCPR	TKGRYSLDVWS	677
	* * *	

Fig. 4-4

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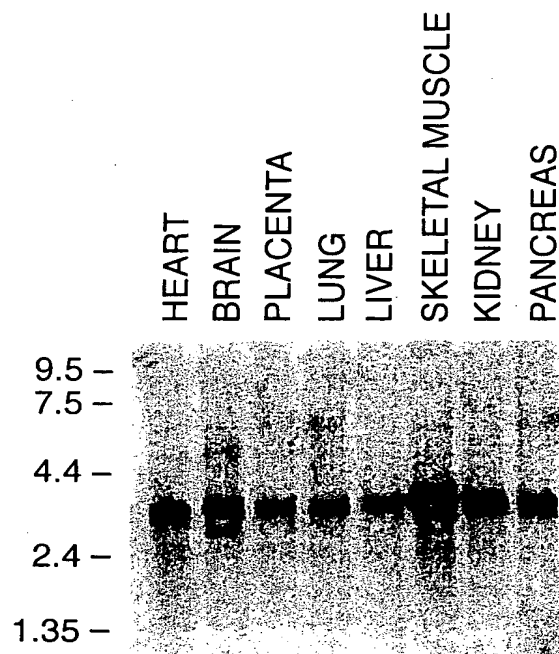


Fig. 5A



Fig. 5B

REPLACEMENT SHEET

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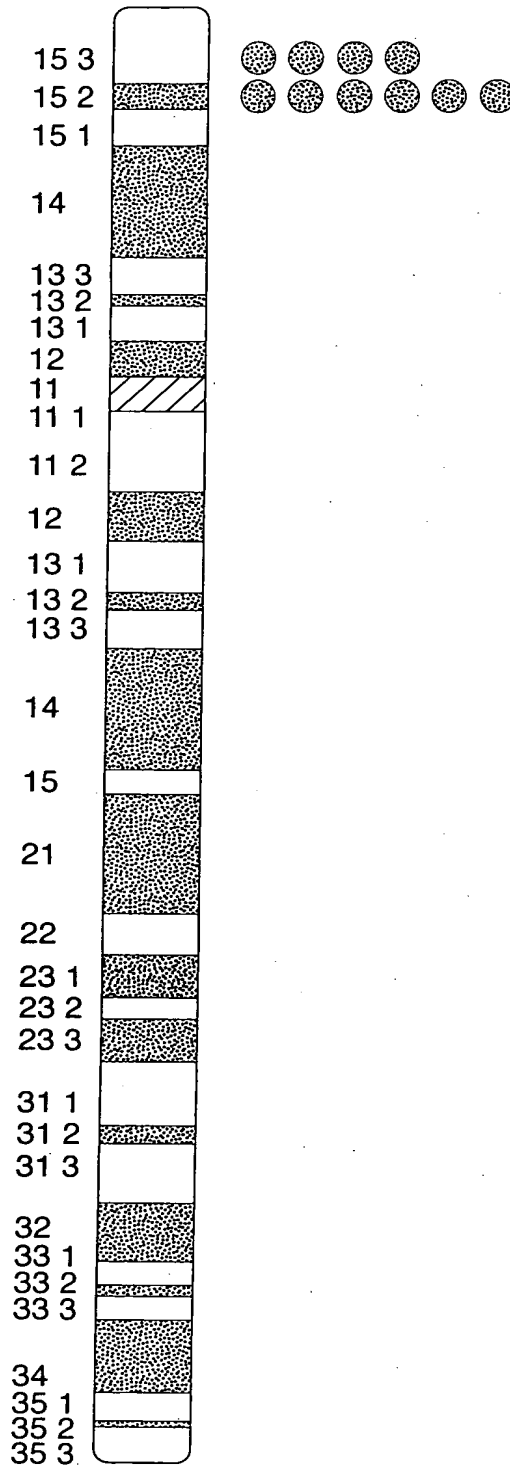


Fig. 6

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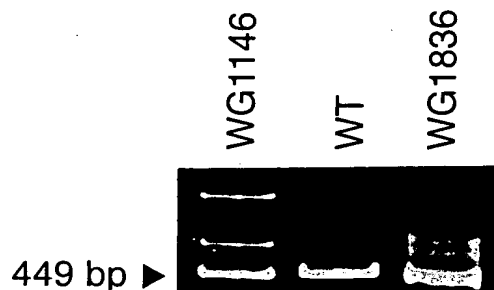


Fig. 7A

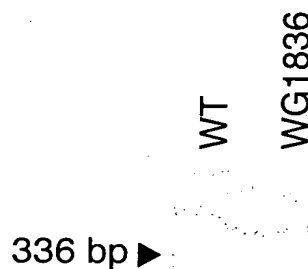


Fig. 7B

Position	Sequence	Accession#	Protein	Organism
572	GAMW [▲] FFGCRHKDRDYLF	(AF025794)	MTRR	(H sapiens)
558	GETLLYYGCRRSDEDYLY	(A60557)	CPR	(H sapiens)
559	GETLLYYGCRRAAEDYLY	(D00101)	CPR	(O cuniculus)
560	GESILYFGCRKRSEDYIY	(X93090)	CPR	(D melanogaster)
572	GPALLFFGCRNRQMDFIY	(P37116)	CPR	(V radiata)
573	GPTVLFFGCRKSDEDFLY	(Z26938)	CPR	(A niger)
1281	CPMVLVFGCRQSKIDHIY	(D16408)	NOS I	(H sapiens)
1009	GRMTLVFGCRRPDEDHIY	(U05810)	NOS II	(H sapiens)
1040	TPMTLVFGCRCSQLDHLY	(L26914)	NOS III	(H sapiens)
380	GRMTLVFGCRHPPEEDHLY	(U85094)	NOS	(O cuniculus)
1005	GDMILLFGCRHPDMDHIY	(U46504)	NOS	(G gallus)
481	GKNWLFFGNPHFTEDFLY	(M23008)	SR	(E coli)
915	GEVFLYLGSRHKREEYLY	(L26503)	SR	(S cerevisiae)
407	GRNWLIFGNRHFHRDFLY	(Z23169)	SR	(T roseopersicina)
261	GLAWLFLGVANVDSLLYD	(X99419)	FNR	(P sativum)
251	GLAWLFLGVPTSSSLLYK	(P00455)	FNR	(S oleracea)

Fig. 7C

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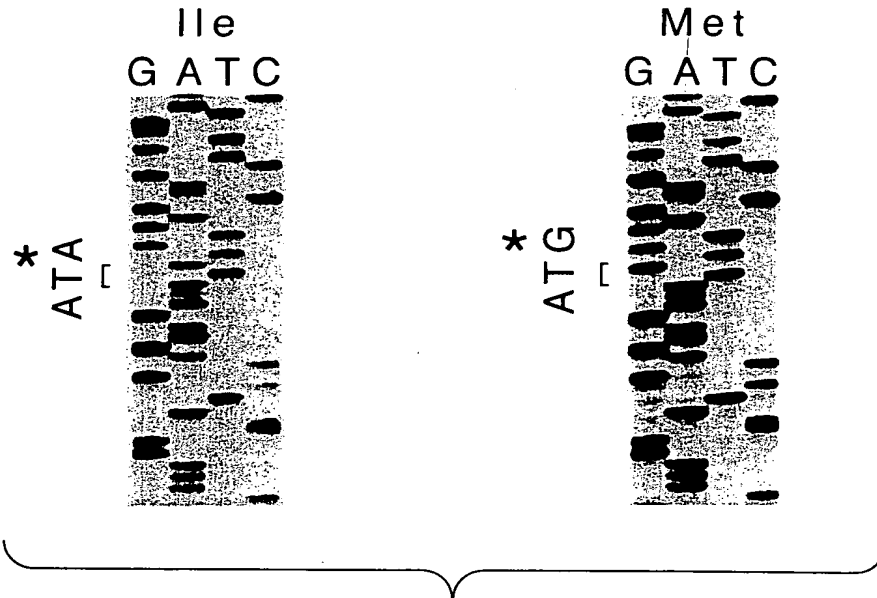


Fig. 8A

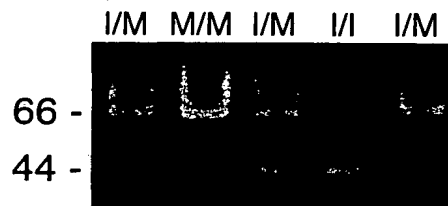


Fig. 8B